GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 07:31:31 ; Search time 299 Seconds
(without alignments)
1431.036 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 190
Sequence: 1 MMNFQPPSKAWRASQMMTFF.....HDGSLDLRSRRSVQEGNPRA 190

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 4

Total number of hits satisfying chosen parameters: 1316744

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=oligna.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=4 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09895298_@CGN_1_1_79_@runat_06112002_160752_3557 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
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24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		190	100.0	1097	22	ABA08605	Human LAK-4p homol
2		190	100.0	1097	22	AAK53221	Human polynucleoti
3		190	100.0	1219	22	AAF82463	Human CASB6411-rel
4		190	100.0	1312	22	AAK52237	Human polynucleoti
5		190	100.0	1461	21	AAA78402	Human secreted pro
6		190	100.0	1813	22	AAH18131	Human cDNA sequenc
7		190	100.0	1960	22	AAF82462	Human CASB6411-rel
8		190	100.0	2243	21	AAA64684	cDNA encoding a hu
9		190	100.0	2407	22	AAF82460	Human CASB6411 cDN
10		190	100.0	2521	22	AAF82461	Alternatively spli
11		150	78.9	1194	23	ABV22463	Human prostate exp
12		150	78.9	1194	23	ABV25683	Human prostate exp
13		150	78.9	1194	23	ABV28278	Human prostate exp
14		120	63.2	470	22	AAL18591	Human breast cance
15		110	57.9	501	22	AAL09919	Human breast cance
16	c	71	37.4	286	23	ABV08852	Human prostate exp
17		71	37.4	617	23	ABV12915	Human prostate exp
18		52	27.4	590	23	ABV34041	Human prostate exp
19		52	27.4	590	23	ABV42908	Human prostate exp
20		50	26.3	777	22	AAH08034	Human cDNA clone (
21		46	24.2	197	22	AAL19767	Human breast cance
22		40	21.1	555	22	AAL20351	Human breast cance
23		35	18.4	454	22	ABA58847	Human foetal liver
24		35	18.4	454	22	AAK07004	Human brain expres
25		35	18.4	454	22	AAK32745	Human bone marrow
26		35	18.4	454	22	AAI38558	Probe #7244 used t
27		35	18.4	454	24	ABS07543	Human genome-deriv
28		34	17.9	233	22	AAL10187	Human breast cance
29		32	16.8	498	22	AAL11452	Human breast cance
30		31	16.3	94	22	ABA71379	Human foetal liver
31		31	16.3	94	22	AAK19696	Human brain expres
32		31	16.3	94	22	AAK45716	Human bone marrow
33		31	16.3	94	22	AAI51641	Probe #20327 used
34		31	16.3	94	24	ABS19993	Human genome-deriv
35		29	15.3	523	23	ABV03746	Human prostate exp
36		16	8.4	402	22	AAF65737	Novel human polynu
37	c	16	8.4	617	22	AAL11030	Human breast cance
38	c	16	8.4	618	22	AAL18794	Human breast cance
39	c	12	6.3	775	22	AAL20104	Human breast cance
40		9	4.7	285	16	AAT25867	Human gene signatu
41		9	4.7	330	22	AAS04641	Gene expression pr
42		9	4.7	506	24	ABQ32690	Oligonucleotide fo
43	c	9	4.7	506	24	ABQ32691	Oligonucleotide fo
44	c	9	4.7	1391	21	AAC77219	Human ORFX ORF2774
45	c	9	4.7	1399	22	AAH48003	Ribosomal S9 prote

ALIGNMENTS

RESULT 1
ABA08605
ID ABA08605 standard; cDNA; 1097 BP.
XX
AC ABA08605;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human LAK-4p homologue-encoding cDNA, SEQ ID NO:381.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11361.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 1; Page 473; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 1097 BP; 288 A; 246 C; 247 G; 316 T; 0 other;

Alignment Scores:

Pred. No.:	2.13e-183	Length:	1097
Score:	190.00	Matches:	190
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-895-298A-83 (1-190) x ABA08605 (1-1097)

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Qy     21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
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Db    329 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 388

Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
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Db    389 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 448

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
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Db    449 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 508

Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
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Db    509 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 568

Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
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Db    569 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 628

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
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Db    629 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 688

Qy    141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
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Db    689 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 748

Qy    161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
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Db    749 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 808

Qy    181 ArgSerValGlnGluGlyAsnProArgAla 190
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Db    809 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 838
```

RESULT 2
AAK53221
ID AAK53221 standard; cDNA; 1097 BP.
XX
AC AAK53221;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2750.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR P-PSDB; AAM80088.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 1; Page 4962; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 1097 BP; 288 A; 246 C; 247 G; 316 T; 0 other;

Alignment Scores:

Pred. No.:	2.13e-183	Length:	1097
Score:	190.00	Matches:	190
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-895-298A-83 (1-190) x AAK53221 (1-1097)

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Db    269 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 328

Qy     21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
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Db    329 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 388

Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
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Db    389 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 448

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
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Db    449 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 508

Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
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Db    509 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 568

Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
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Db    569 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 628

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
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Qy    141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
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Db    689 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 748

Qy    161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
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Db    749 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 808

Qy    181 ArgSerValGlnGluGlyAsnProArgAla 190
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Db    809 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 838
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RESULT 3
AAF82463
ID AAF82463 standard; cDNA; 1219 BP.
XX
AC AAF82463;
XX
DT 29-JUN-2001 (first entry)
XX
DE Human CASB6411-related cDNA #2.
XX
KW Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
KW ovarian cancer; colon cancer; autoimmune disease; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
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FT		/partial
FT		/note= "this sequence does not contain a start codon"

XX
PN WO200123417-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-EP09500.
XX
PR 30-SEP-1999; 99GB-0023154.
PR 07-JUL-2000; 2000GB-0016839.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Vinals De Bassols YC;
XX
DR WPI; 2001-316133/33.
DR P-PSDB; AAB83082.
XX
PT Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
PT prophylactic and therapeutic treatment of cancers, particularly ovarian
PT and colon cancers, autoimmune diseases and related conditions -
XX
PS Claim 32; Page 66-67; 95pp; English.
XX
CC The present sequence is provided in a specification relating
CC to CASB6411 polypeptides comprising a sequence having at least 70%
CC identity to a sequence of 460 or 154 amino acids fully defined in
CC the specification. CASB6411 polypeptides and polynucleotides are
CC useful for treating a subject by immunoprophylaxis or therapy.
CC The CASB6411 polypeptides are useful in diagnostics, and as
CC vaccines for prophylactic and therapeutic treatment of cancers,
CC particularly ovarian and colon cancers, autoimmune diseases and related
CC conditions. CASB6411 polypeptides are also useful for the
CC structure-based design of agonists, antagonists or inhibitors of the
CC polypeptide.
XX
SQ Sequence 1219 BP; 346 A; 260 C; 275 G; 338 T; 0 other;

Alignment Scores:

Pred. No.:	2.36e-183	Length:	1219

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Score:                  190.00        Matches:       190
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     22            Gaps:          0

US-09-895-298A-83 (1-190) x AAF82463 (1-1219)

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Qy     21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
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Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 183

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
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Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
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Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
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Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 423

Qy    141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 483

Qy    161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 543

Qy    181 ArgSerValGlnGluGlyAsnProArgAla 190
          ||||||||||||||||||||||||||||||
Db    544 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 573

RESULT 4
AAK52237
ID   AAK52237 standard; cDNA; 1312 BP.
XX
AC   AAK52237;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 782.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79104.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 2615-2616; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 1312 BP; 370 A; 286 C; 287 G; 369 T; 0 other;

Alignment Scores:
Pred. No.:              2.53e-183     Length:        1312
Score:                  190.00        Matches:       190
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     22            Gaps:          0

US-09-895-298A-83 (1-190) x AAK52237 (1-1312)

Qy      1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    294 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 353

Qy     21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    354 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 413

Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    414 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 473

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    474 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 533

Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 593

Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    594 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 653

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     654 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 713

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     714 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 773

Qy     161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     774 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 833

Qy     181 ArgSerValGlnGluGlyAsnProArgAla 190
            ||||||||||||||||||||||||||||||
Db     834 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 863

RESULT 5
AAA78402
ID   AAA78402 standard; cDNA; 1461 BP.
XX
AC   AAA78402;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human secreted protein gene 22 SEQ ID NO:32.
XX
KW   Human; secreted protein; cytostatic; antianaemic; antidiabetic;
KW   antiinflammatory; ophthalmological; antirheumatic; antiarthritic;
KW   antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic;
KW   neuroprotective; antimicrobial; antiparkinsonian; cancer;
KW   immune system disorder; angiogenesis; hyperproliferative disorder;
KW   cardiovascular disorder; apoptosis; neurological disease;
KW   infectious disease; wound healing; ss.
XX
OS   Homo sapiens.
XX
PN   WO200035937-A1.
XX
PD   22-JUN-2000.
XX
PF   16-DEC-1999;   99WO-US29950.
XX
PR   17-DEC-1998;   98US-0112809.
PR   18-DEC-1998;   98US-0113006.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ebner R,  Rosen CA,  Endress GA,  Soppet DR,  Ni J;
PI   Duan DR,  Moore PA,  Shi Y,  Lafleur DW,  Olsen HS,  Florence K;
XX
DR   WPI; 2000-431566/37.
DR   P-PSDB; AAB24458.
XX
PT   Forty seven human nucleic acids encoding secreted proteins, useful in
PT   the treatment, prevention and diagnosis of cancers, disorders of the
PT   immune system, angiogenesis disorders, neurological diseases and
PT   hyperproliferative disorders -
XX
PS   Claim 1; Page 457-458; 562pp; English.
XX
CC   The polynucleotide sequence given in AAA78381 to AAA78432 encode the
CC   human secreted proteins given in AAB24437 to AAB24604. Human secreted
CC   proteins have activities based on the tissues and cells the genes are
CC   expressed in. Examples of activities include: cytostatic; antianaemic;
CC   antidiabetic; antiinflammatory; ophthalmological; antirheumatic;
CC   antiarthritic; antipsoriatic; antiangiogenic; cardiant; anti-HIV;
CC   nootropic; neuroprotective; antimicrobial and antiparkinsonian.
CC   Human secreted protein polynucleotides, polypeptides, antagonists and/or
CC   agonists may be useful in treating, preventing, and/or diagnosing other
CC   diseases, disorders, and/or conditions such as: (a) cancers; (b)
CC   disorders of the immune system; (c) angiogenesis disorders; (d)
CC   hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases
CC   associated with increase apoptosis; (g) neurological diseases; and
CC   (h) infectious diseases. They are also used to promote wound healing.
CC   AAA78372 to AAA78380 and AAB24436 represent sequences used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 1461 BP; 428 A; 312 C; 324 G; 397 T; 0 other;

Alignment Scores:
Pred. No.:                2.81e-183      Length:          1461
Score:                    190.00         Matches:         190
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-895-298A-83 (1-190) x AAA78402 (1-1461)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 122

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 ATCTTCTTGCTCTTTTTCCCATCTTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 182

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 242

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 302

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 362

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 422

Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 482

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     483 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 542

Qy     161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     543 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 602

Qy     181 ArgSerValGlnGluGlyAsnProArgAla 190
             ||||||||||||||||||||||||||||||
Db     603 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 632

RESULT 6
AAH18131
ID   AAH18131 standard; cDNA; 1813 BP.
XX
AC   AAH18131;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:18001.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
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PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 18001; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 1813 BP; 489 A; 400 C; 405 G; 519 T; 0 other;

Alignment Scores:
Pred. No.:                3.46e-183      Length:          1813
Score:                    190.00         Matches:         190
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       22             Gaps:            0

US-09-895-298A-83 (1-190) x AAH18131 (1-1813)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 510

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 570

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     571 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 630

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     631 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 690

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 750

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 810

Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 870

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 930

Qy     161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 990

Qy     181 ArgSerValGlnGluGlyAsnProArgAla 190
           ||||||||||||||||||||||||||||||
Db     991 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 1020

RESULT 7
AAF82462
ID   AAF82462 standard; cDNA; 1960 BP.
XX
AC   AAF82462;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Human CASB6411-related cDNA #1.
XX
KW   Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
KW   ovarian cancer; colon cancer; autoimmune disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1317
FT                   /*tag= a
FT                   /partial
FT                   /note= "this sequence does not contain a start codon"
XX
PN   WO200123417-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-EP09500.
XX
PR   30-SEP-1999;   99GB-0023154.
PR   07-JUL-2000; 2000GB-0016839.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Vinals De Bassols YC;
XX
DR   WPI; 2001-316133/33.
DR   P-PSDB; AAB83081.
XX
PT   Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
PT   prophylactic and therapeutic treatment of cancers, particularly ovarian
PT   and colon cancers, autoimmune diseases and related conditions -
XX
PS   Claim 32; Page 65-66; 95pp; English.
XX
CC   The present sequence is provided in a specification relating
CC   to CASB6411 polypeptides comprising a sequence having at least 70%
CC   identity to a sequence of 460 or 154 amino acids fully defined in
CC   the specification. CASB6411 polypeptides and polynucleotides are
CC   useful for treating a subject by immunoprophylaxis or therapy.
CC   The CASB6411 polypeptides are useful in diagnostics, and as
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CC   vaccines for prophylactic and therapeutic treatment of cancers,
CC   particularly ovarian and colon cancers, autoimmune diseases and related
CC   conditions. CASB6411 polypeptides are also useful for the
CC   structure-based design of agonists, antagonists or inhibitors of the
CC   polypeptide.
XX
SQ   Sequence 1960 BP; 515 A; 439 C; 447 G; 559 T; 0 other;

Alignment Scores:
Pred. No.:                3.73e-183      Length:          1960
Score:                    190.00         Matches:         190
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       22             Gaps:            0

US-09-895-298A-83 (1-190) x AAF82462 (1-1960)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     745 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 804

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     805 ATCTTCTTGCTCTTTTTCCCATCTTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 864

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     865 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 924

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     925 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 984

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     985 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTG 1044

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1045 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 1104

Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1105 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 1164

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1165 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 1224

Qy     161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1225 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 1284

Qy     181 ArgSerValGlnGluGlyAsnProArgAla 190
           ||||||||||||||||||||||||||||||
Db    1285 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 1314

RESULT 8
AAA64684
ID   AAA64684 standard; cDNA; 2243 BP.
XX
AC   AAA64684;
XX
DT   02-JAN-2001  (first entry)
XX
DE   cDNA encoding a human leukocyte and blood related protein (LBAP).
XX
KW   Human; leukocyte and blood related protein; LBAP; arteriosclerosis;
KW   cell proliferative disorder; actinic keratosis; atherosclerosis;
KW   bursitis; cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
KW   myelofibrosis; paroxysmal nocturnal hemoglobinuria; cancer;
KW   adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma;
KW   teratocarcinoma; autoimmune disorder; inflammatory disorder;
KW   acquired immunodeficiency syndrome; AIDS; Addison's disease;
KW   adult respiratory distress syndrome; allergy; ankylosing spondylitis;
KW   amyloidosis; anaemia; asthma; autoimmune haemolytic anaemia; infection;
KW   Werner syndrome; haemodialysis; extracorporeal circulation; trauma; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             109..1272
FT                   /*tag=  a
FT                   /product= "leukocyte and blood related protein (LBAP)"
FT   sig_peptide     109..261
FT                   /*tag=  b
XX
PN   WO200052161-A2.
XX
PD   08-SEP-2000.
XX
PF   29-FEB-2000; 2000WO-US05153.
XX
PR   01-MAR-1999;   99US-0122080.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P,  Yue H,  Hillman JL,  Lu DAM,  Baughn MR,  Tang YT,  Azimzai Y;
XX
DR   WPI; 2000-587310/55.
DR   P-PSDB; AAB08764.
XX
PT   Leukocyte and blood associated proteins and polynucleotides encoding
PT   them, useful for diagnosis, treatment and prevention of
PT   autoimmune/inflammatory disorders and cell proliferative disorders
PT   including cancer -
XX
PS   Claim 4; Page 68-69; 70pp; English.
XX
CC   The present sequence encodes a human leukocyte and blood related
CC   protein, designated LBAP. LBAP polynucleotides and polypeptides are
CC   useful for treating or preventing a disorder associated with decreased
CC   expression or activity of LBAP including a cell proliferative disorder
CC   such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,
CC   cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
CC   myelofibrosis, paroxysmal nocturnal hemoglobinuria, etc., cancers
CC   including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma,
CC   sarcoma, teratocarcinoma and in particular cancers of the adrenal
CC   gland, bladder, bone, bone marrow, brain, breast, cervix, etc., and
CC   an autoimmune/inflammatory disorder such as acquired immunodeficiency
CC   syndrome (AIDS), Addison's disease, adult respiratory distress syndrome,
CC   allergies, ankylosing spondylitis, amyloidosis, anaemia, asthma,
CC   atherosclerosis, autoimmune haemolytic anaemia, etc., Werner syndrome,
CC   complications of cancer, haemodialysis, and extracorporeal circulation,
CC   viral, bacterial, fungal, parasitic, protozoan, and helminthic
CC   infections, and trauma.
XX
SQ   Sequence 2243 BP; 602 A; 500 C; 520 G; 621 T; 0 other;

Alignment Scores:
Pred. No.:                4.25e-183      Length:          2243
Score:                    190.00         Matches:         190
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-895-298A-83 (1-190) x AAA64684 (1-2243)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 759

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    760 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 819

Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 879

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 939

Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 999

Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 1059

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 1119

Qy    141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 1179

Qy    161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 1239

Qy    181 ArgSerValGlnGluGlyAsnProArgAla 190
          ||||||||||||||||||||||||||||||
Db   1240 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 1269

RESULT 9
AAF82460
ID   AAF82460 standard; cDNA; 2407 BP.
XX
AC   AAF82460;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Human CASB6411 cDNA.
XX
KW   Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
KW   ovarian cancer; colon cancer; autoimmune disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             382..1764
FT                   /*tag= a
FT                   /product= "CASB6411"
XX
PN   WO200123417-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-EP09500.
XX
PR   30-SEP-1999;   99GB-0023154.
PR   07-JUL-2000; 2000GB-0016839.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Vinals De Bassols YC;
XX
DR   WPI; 2001-316133/33.
DR   P-PSDB; AAB83079.
XX
PT   Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
PT   prophylactic and therapeutic treatment of cancers, particularly ovarian
PT   and colon cancers, autoimmune diseases and related conditions -
XX
PS   Claim 11; Page 63-64; 95pp; English.
XX
CC   The present sequence encodes human CASB6411 polypeptide. The
CC   invention relates to CASB6411 polypeptides comprising a sequence
CC   having at least 70% identity to a sequence of 460 or 154 amino acids
CC   fully defined in the specification. CASB6411 polypeptides and
CC   polynucleotides are useful for treating a subject by immunoprophylaxis
CC   or therapy. The CASB6411 polypeptides are useful in diagnostics, and
CC   as vaccines for prophylactic and therapeutic treatment of cancers,
CC   particularly ovarian and colon cancers, autoimmune diseases and related
CC   conditions. CASB6411 polypeptides are also useful for the
CC   structure-based design of agonists, antagonists or inhibitors of the
CC   polypeptide.  The present sequence may be alternatively spliced to
CC   generate a sequence encoding a truncated CASB6411 protein.
XX
SQ   Sequence 2407 BP; 635 A; 557 C; 546 G; 669 T; 0 other;

Alignment Scores:
Pred. No.:              4.55e-183     Length:          2407
Score:                  190.00        Matches:         190
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            100.00%       Indels:          0
DB:                     22            Gaps:            0

US-09-895-298A-83 (1-190) x AAF82460 (1-2407)

Qy      1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1192 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 1251

Qy     21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1252 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 1311

Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1312 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 1371

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1372 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 1431

Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1432 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 1491

Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1492 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 1551

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1552 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 1611

Qy    141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1612 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 1671

Qy    161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1672 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 1731

Qy    181 ArgSerValGlnGluGlyAsnProArgAla 190
          ||||||||||||||||||||||||||||||
Db   1732 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 1761

RESULT 10
AAF82461
ID   AAF82461 standard; cDNA; 2521 BP.
XX
AC   AAF82461;
```

```
XX
DT   29-JUN-2001  (first entry)
XX
DE   Alternatively spliced human CASB6411 cDNA encoding truncated protein.
XX
KW   Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
KW   ovarian cancer; colon cancer; autoimmune disease; isoform;
KW   alternative splicing; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             382..846
FT                   /*tag=  a
FT                   /product= "truncated CASB6411"
XX
PN   WO200123417-A2.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000WO-EP09500.
XX
PR   30-SEP-1999;   99GB-0023154.
PR   07-JUL-2000; 2000GB-0016839.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Vinals De Bassols YC;
XX
DR   WPI; 2001-316133/33.
DR   P-PSDB; AAB83080.
XX
PT   Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
PT   prophylactic and therapeutic treatment of cancers, particularly ovarian
PT   and colon cancers, autoimmune diseases and related conditions  -
XX
PS   Claim 11; Page 64-65; 95pp; English.
XX
CC   The present sequence encodes a truncated CASB6411 polypeptide. It
CC   is generated by alternative splicing of the full length human cDNA
CC   sequence of CASB6411. The invention relates to CASB6411 polypeptides
CC   comprising a sequence having at least 70% identity to a sequence of
CC   460 or 154 amino acids fully defined in the specification. CASB6411
CC   polypeptides and polynucleotides are useful for treating a subject by
CC   immunoprophylaxis or therapy. The CASB6411 polypeptides are useful in
CC   diagnostics, and as vaccines for prophylactic and therapeutic treatment
CC   of cancers, particularly ovarian and colon cancers, autoimmune diseases
CC   and related conditions. CASB6411 polypeptides are also useful for the
CC   structure-based design of agonists, antagonists or inhibitors of the
CC   polypeptide.
XX
SQ   Sequence 2521 BP; 662 A; 583 C; 583 G; 693 T; 0 other;

Alignment Scores:
Pred. No.:              4.76e-183      Length:         2521
Score:                  190.00         Matches:        190
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     22             Gaps:           0

US-09-895-298A-83 (1-190) x AAF82461 (1-2521)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1306 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 1365

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1366 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 1425

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1426 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 1485

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1486 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 1545

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1546 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 1605

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1606 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 1665

Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1666 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 1725

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1726 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 1785

Qy     161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1786 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 1845

Qy     181 ArgSerValGlnGluGlyAsnProArgAla 190
           ||||||||||||||||||||||||||||||
Db    1846 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 1875

RESULT 11
ABV22463
ID   ABV22463 standard; cDNA; 1194 BP.
XX
AC   ABV22463;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 22454.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 3912; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
```

```
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:
Pred. No.:                1.05e-142      Length:          1194
Score:                    150.00         Matches:         150
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              78.95%         Indels:          0
DB:                       23             Gaps:            0

US-09-895-298A-83 (1-190) x ABV22463 (1-1194)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     531 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 590

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     591 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 650

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     651 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 710

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     711 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 770

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     771 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 830

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     831 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 890

Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     891 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 950

Qy     141 LeuGlnAspMetGluLysLysAlaAsnPro 150
           |||||||||||||||||||||||||||||
Db     951 CTGCAGGATATGGAGAAGAAAGCAAACCCA 980

RESULT 12
ABV25683
ID   ABV25683 standard; cDNA; 1194 BP.
XX
AC   ABV25683;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 25674.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 5146-5147; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:
Pred. No.:                1.05e-142      Length:          1194
Score:                    150.00         Matches:         150
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              78.95%         Indels:          0
DB:                       23             Gaps:            0

US-09-895-298A-83 (1-190) x ABV25683 (1-1194)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     531 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 590

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     591 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 650

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     651 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 710

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     711 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 770

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     771 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 830

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    831 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 890

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    891 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 950

Qy    141 LeuGlnAspMetGluLysLysAlaAsnPro 150
          |||||||||||||||||||||||||||||
Db    951 CTGCAGGATATGGAGAAGAAAGCAAACCCA 980

RESULT 13
ABV28278
ID   ABV28278 standard; cDNA; 1194 BP.
XX
AC   ABV28278;
XX
DT   16-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 28269.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 5881-5882; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:
Pred. No.:              1.05e-142      Length:        1194
Score:                  150.00         Matches:       150
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            78.95%         Indels:        0
DB:                     23             Gaps:          0

US-09-895-298A-83 (1-190) x ABV28278 (1-1194)

Qy      1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    531 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 590

Qy     21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    591 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 650

Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    651 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 710

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    711 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 770

Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    771 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 830

Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    831 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 890

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    891 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 950

Qy    141 LeuGlnAspMetGluLysLysAlaAsnPro 150
          |||||||||||||||||||||||||||||
Db    951 CTGCAGGATATGGAGAAGAAAGCAAACCCA 980

RESULT 14
AAL18591
ID   AAL18591 standard; cDNA; 470 BP.
XX
AC   AAL18591;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human breast cancer expressed polynucleotide 11048.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628-A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US00798.
XX
PR   14-JAN-2000; 2000US-0176077.
PR   14-MAR-2000; 2000US-0189167.
PR   24-MAR-2000; 2000US-0192099.
PR   29-MAR-2000; 2000US-0193480.
PR   15-MAY-2000; 2000US-0205230.
PR   09-JUN-2000; 2000US-0211315.
PR   25-JUL-2000; 2000US-0220534.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer  -
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XX
PS   Claim 1; Page 1968; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity.
XX
SQ   Sequence 470 BP; 144 A; 92 C; 116 G; 118 T; 0 other;

Alignment Scores:
Pred. No.:              1.32e-112      Length:         470
Score:                  120.00         Matches:        120
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            63.16%         Indels:         0
DB:                     22             Gaps:           0

US-09-895-298A-83 (1-190) x AAL18591 (1-470)

Qy      71 ThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerValHis 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5 ACACGGCCTGGCTACCTGTGGGTTGTTTGGATCTATCGGAACCTCATTGGAAGTGTGCAC 64

Qy      91 PhePhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrpGlnIleThr 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 TTCTTTTTCATCCTCACCCTCATTGTGCTAATCATCACCTATCTTTACTGGCAGATCACA 124

Qy     111 GluGlyArgLysIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLysAsp 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 GAGGGAAGGAAGATTATGATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAAGAT 184

Qy     131 LysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsnPro 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 AAAATGTTCCTGATAGAAAAATTGATCAAGCTGCAGGATATGGAGAAGAAAGCAAACCCC 244

Qy     151 SerSerLeuValLeuGluArgArgGluValGluGlnGlnGlyPheLeuHisLeuGlyGlu 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 AGCTCACTTGTTCTGGAAAGGAGAGAGGTGGAGCAACAAGGCTTTTTGCATTTGGGGGAA 304

Qy     171 HisAspGlySerLeuAspLeuArgSerArgArgSerValGlnGluGlyAsnProArgAla 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 CATGATGGCAGTCTTGACTTGCGATCTAGAAGATCAGTTCAAGAAGGTAATCCAAGGGCC 364

RESULT 15
AAL09919
ID   AAL09919 standard; cDNA; 501 BP.
XX
AC   AAL09919;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human breast cancer expressed polynucleotide 2376.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628-A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US00798.
XX
PR   14-JAN-2000; 2000US-0176077.
PR   14-MAR-2000; 2000US-0189167.
PR   24-MAR-2000; 2000US-0192099.
PR   29-MAR-2000; 2000US-0193480.
PR   15-MAY-2000; 2000US-0205230.
PR   09-JUN-2000; 2000US-0211315.
PR   25-JUL-2000; 2000US-0220534.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer  -
XX
PS   Claim 1; Page 455; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity.
XX
SQ   Sequence 501 BP; 147 A; 101 C; 128 G; 122 T; 3 other;

Alignment Scores:
Pred. No.:              2.04e-102      Length:         501
Score:                  110.00         Matches:        110
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            57.89%         Indels:         0
DB:                     22             Gaps:           0

US-09-895-298A-83 (1-190) x AAL09919 (1-501)

Qy      71 ThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerValHis 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36 ACACGGCCTGGCTACCTGTGGGTTGTTTGGATCTATCGGAACCTCATTGGAAGTGTGCAC 95

Qy      91 PhePhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrpGlnIleThr 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 TTCTTTTTCATCCTCACCCTCATTGTGCTAATCATCACCTATCTTTACTGGCAGATCACA 155

Qy     111 GluGlyArgLysIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLysAsp 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GAGGGAAGGAAGATTATGATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAAGAT 215

Qy     131 LysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsnPro 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AAAATGTTCCTGATAGAAAAATTGATCAAGCTGCAGGATATGGAGAAGAAAGCAAACCCC 275

Qy     151 SerSerLeuValLeuGluArgArgGluValGluGlnGlnGlyPheLeuHisLeuGlyGlu 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 AGCTCACTTGTTCTGGAAAGGAGAGAGGTGGAGCAACAAGGCTTTTTGCATTTGGGGGAA 335

Qy     171 HisAspGlySerLeuAspLeuArgSerArg 180
           |||||||||||||||||||||||||||||
Db     336 CATGATGGCAGTCTTGACTTGCGATCTAGA 365


Search completed: November  9, 2002, 07:45:52
Job time : 305 secs
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